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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=9; day=18; hr=11; min=52; sec=58; ms=505;]

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Application No: 10583110 Version No: 2.0

Input Set:**Output Set:**

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Finished: 2008-08-20 09:59:52.931
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 589 ms
Total Warnings: 69
Total Errors: 0
No. of SeqIDs Defined: 70
Actual SeqID Count: 70

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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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Input Set:

Output Set:

Started: 2008-08-20 09:59:50.342
Finished: 2008-08-20 09:59:52.931
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 589 ms
Total Warnings: 69
Total Errors: 0
No. of SeqIDs Defined: 70
Actual SeqID Count: 70

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (69)
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SEQUENCE LISTING

<110> TANAKA, YOSHIKAZU
 ONO, EIICHIRO
 NAKAMURA, NORIKO
 MIZUTANI, MASAKO

<120> METHOD FOR PRODUCING YELLOW FLOWER BY CONTROLLING
 FLAVONOID SYNTHETIC PATHWAY

<130> 47237.5008/00US

<140> 10583110

<141> 2008-08-20

<150> PCT/JP2004/019461

<151> 2004-12-17

<150> JP 2003-420046

<151> 2003-12-17

<160> 70

<170> PatentIn Ver. 3.3

<210> 1

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1371)

<220>

<223> Description of Artificial Sequence: Synthetic
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gaa gaa cac ctc aac tct tca ata gcc ctt gca aag ttc ata acc aaa	96
Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys	
20 25 30	

cac cac tct tca atc tcc atc act atc atc agc act gcc ccc gcc gaa	144
His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu	
35 40 45	

tct tct gaa gtg gcc aaa att att aat aat ccg tca ata act tac cgc	192
Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg	
50 55 60	

ggc ctc acc gcg gta gcg ctc cct gaa aat ctc acc agt aac att aat	240
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Gly	Leu	Thr	Ala	Val	Ala	Leu	Pro	Glu	Asn	Leu	Thr	Ser	Asn	Ile	Asn	
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aaa	aac	ccc	gtc	gaa	ctt	ttc	ttc	gaa	atc	cct	cgt	cta	caa	aac	gcc	288
Lys	Asn	Pro	Val	Glu	Leu	Phe	Phe	Glu	Ile	Pro	Arg	Leu	Gln	Asn	Ala	
			85					90					95			
aac	ctt	cga	gag	gct	tta	cta	gat	att	tcg	cga	aaa	tcc	gat	atc	aaa	336
Asn	Leu	Arg	Glu	Ala	Leu	Leu	Asp	Ile	Ser	Arg	Lys	Ser	Asp	Ile	Lys	
		100					105					110				
gca	tta	atc	atc	gat	ttc	ttc	tgc	aat	gcg	gca	ttt	gaa	gta	tcc	acc	384
Ala	Leu	Ile	Ile	Asp	Phe	Phe	Cys	Asn	Ala	Ala	Phe	Glu	Val	Ser	Thr	
	115					120					125					
agc	atg	aac	ata	ccc	act	tac	ttc	gac	gtc	agt	ggc	ggc	gct	ttt	ctc	432
Ser	Met	Asn	Ile	Pro	Thr	Tyr	Phe	Asp	Val	Ser	Gly	Gly	Ala	Phe	Leu	
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ctc	tgc	acg	ttt	ctc	cac	cac	ccg	aca	cta	cac	caa	act	gtt	cgt	gga	480
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Asp	Ile	Ala	Asp	Leu	Asn	Asp	Ser	Val	Glu	Met	Pro	Gly	Phe	Pro	Leu	
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att	cac	tcc	tct	gat	tta	cca	atg	agt	ttg	ttt	tat	cgt	aag	act	aat	576
Ile	His	Ser	Ser	Asp	Leu	Pro	Met	Ser	Leu	Phe	Tyr	Arg	Lys	Thr	Asn	
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gtt	tac	aaa	cac	ttt	cta	gac	act	tcc	tta	aac	atg	cgc	aaa	tcg	agt	624
Val	Tyr	Lys	His	Phe	Leu	Asp	Thr	Ser	Leu	Asn	Met	Arg	Lys	Ser	Ser	
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ggg	ata	ctc	gtg	aac	acg	ttt	gtt	gcg	ctc	gag	ttt	cga	gct	aag	gaa	672
Gly	Ile	Leu	Val	Asn	Thr	Phe	Val	Ala	Leu	Glu	Phe	Arg	Ala	Lys	Glu	
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gct	ttg	tcc	aac	ggg	ttg	tac	ggg	cca	act	ccg	cct	ctt	tat	tta	ctt	720
Ala	Leu	Ser	Asn	Gly	Leu	Tyr	Gly	Pro	Thr	Pro	Pro	Leu	Tyr	Leu	Leu	
225				230					235			240				
tca	cat	aca	att	gcc	gaa	ccc	cac	gac	act	aaa	gtg	ttg	gta	aac	caa	768
Ser	His	Thr	Ile	Ala	Glu	Pro	His	Asp	Thr	Lys	Val	Leu	Val	Asn	Gln	
		245					250					255				
cac	gaa	tgc	cta	tca	tgg	ctt	gat	ttg	cag	cct	agt	aaa	agc	gtg	att	816
His	Glu	Cys	Leu	Ser	Trp	Leu	Asp	Leu	Gln	Pro	Ser	Lys	Ser	Val	Ile	
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ttc	ctt	tgt	ttc	gga	aga	aga	gga	gcg	ttc	tca	gca	caa	cag	ttg	aaa	864
Phe	Leu	Cys	Phe	Gly	Arg	Arg	Gly	Ala	Phe	Ser	Ala	Gln	Gln	Leu	Lys	
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Gly	Leu	Thr	Ala	Val	Ala	Leu	Pro	Glu	Asn	Leu	Thr	Ser	Asn	Ile	Asn	65	70	75
Lys	Asn	Pro	Val	Glu	Leu	Phe	Phe	Glu	Ile	Pro	Arg	Leu	Gln	Asn	Ala	85	90	95
Asn	Leu	Arg	Glu	Ala	Leu	Leu	Asp	Ile	Ser	Arg	Lys	Ser	Asp	Ile	Lys	100	105	110
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Leu	Cys	Thr	Phe	Leu	His	His	Pro	Thr	Leu	His	Gln	Thr	Val	Arg	Gly	145	150	155
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His	Glu	Cys	Leu	Ser	Trp	Leu	Asp	Leu	Gln	Pro	Ser	Lys	Ser	Val	Ile	260	265	270
Phe	Leu	Cys	Phe	Gly	Arg	Arg	Gly	Ala	Phe	Ser	Ala	Gln	Gln	Leu	Lys	275	280	285
Glu	Ile	Ala	Ile	Gly	Leu	Glu	Lys	Ser	Gly	Cys	Arg	Phe	Leu	Trp	Leu	290	295	300
Ala	Arg	Ile	Ser	Pro	Glu	Met	Asp	Leu	Asn	Ala	Leu	Leu	Pro	Glu	Gly	305	310	315
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Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val
325 330 335

Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr
340 345 350

His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro
355 360 365

Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe
370 375 380

Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly
385 390 395 400

Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu
405 410 415

Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile
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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 3

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21

<210> 4

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 4

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21

<210> 5

<211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 5
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 <210> 6
 <211> 21
 <212> DNA
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 <223> Description of Artificial Sequence: Synthetic
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 <400> 6
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 <210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic
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 <400> 7
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 <210> 8
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic
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 <400> 8
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 <210> 9
 <211> 21
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic

primer

<400> 9

cacgaatgct tagcatggct c

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<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<400> 10

cttattgccc actgaaaccc c

21

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<400> 11

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<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<400> 12

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21

<210> 13

<211> 1446

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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ttggacatgg ccaagctctt tacctcaaga ggcatacaaa caacaatcat ttcgactctc 120

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actgaagatt ggctcccaaa gtttggtgag tcattagtct tattacaaga gccagttgag 300
aagcttatcg aagaactaaa gctcgactgt ctcgtttccg acatgttctt gccttggaac 360
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1446

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<210> 14

<211> 1488

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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gaatcaggac agtccattcg tcttctccaa gtaaaattcc ctggtgaaga agccgggttg 240
ccacctggat gcgaaagcgc cgagacttta ccatcttatg aattgattcc aaattttttt 300
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cttggtagaaa tggctaagag ggcagtcctaa gttgggggat cttcatgtaa gaatgtcgac 1440
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<210> 15

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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